

IN THE SPECIFICATION

Please insert the following paragraph immediately after the title of the application.

This application is a national stage application filed under 35 U.S.C. § 371 of International Application No. PCT/US00/16668, filed June 16, 2000 and published in English as WO 07/8953A2 on December 28, 2000, which claims the benefit of U.S. Provisional Application No. 60/139,923, filed June 17, 1999, U.S. Provisional Application No. 60/148,177, filed August 10, 1999, U.S. Provisional Application No. 60/149,357, filed August 18, 1999, and U.S. Provisional Application No. 60/162,287, filed October 28, 1999.

Please replace the paragraph beginning at page 20, line 21 with the following amended paragraph:

Alternatively, a suite of commonly used and freely available sequence comparison algorithms is provided by the National Center for Biotechnology Information (NCBI) Basic Local Alignment Search Tool (BLAST) (Altschul, S.F. et al. (1990) J. Mol. Biol. 215:403-410), which is available from several sources, including the NCBI, Bethesda, MD, and on the Internet at ~~<http://www.ncbi.nlm.nih.gov/BLAST/>~~ ncbi.nlm.nih.gov/BLAST/. The BLAST software suite includes various sequence analysis programs including “blastn,” that is used to align a known polynucleotide sequence with other polynucleotide sequences from a variety of databases. Also available is a tool called “BLAST 2 Sequences” that is used for direct pairwise comparison of two nucleotide sequences. “BLAST 2 Sequences” can be accessed and used interactively at ~~<http://www.ncbi.nlm.nih.gov/gorf/bl2.html>~~ ncbi.nlm.nih.gov/gorf/bl2.html. The “BLAST 2 Sequences” tool can be used for both blastn and blastp (discussed below). BLAST programs are commonly used with gap and other parameters set to default settings. For example, to compare two nucleotide sequences, one may use blastn with the “BLAST 2 Sequences” tool Version 2.0.12 (April-21-2000) set at default parameters. Such default parameters may be, for example:

Matrix: BLOSUM62

Reward for match: 1

Penalty for mismatch: -2

Open Gap: 5 and Extension Gap: 2 penalties

Gap x drop-off: 50

Expect: 10

Word Size: 11

Filter: on

Please replace the paragraph beginning at page 65, line 17 with the following amended paragraph:

The genetic map locations of SEQ ID NO:44, SEQ ID NO:48, SEQ ID NO:60, SEQ ID NO:65, SEQ ID NO:69, SEQ ID NO:70, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:76, SEQ ID NO:80, and SEQ ID NO:83 are described in The Invention as ranges, or intervals, of human chromosomes. More than one map location is reported for SEQ ID NO:65, SEQ ID NO:73, SEQ ID NO:80, and SEQ ID NO:83, indicating that previously mapped sequences having similarity, but not complete identity, to SEQ ID NO:65, SEQ ID NO:73, SEQ ID NO:80, and SEQ ID NO:83 were assembled into their respective clusters. The map position of an interval, in centiMorgans, is measured relative to the terminus of the chromosome's p-arm. (The centiMorgan (cM) is a unit of measurement based on recombination frequencies between chromosomal markers. On average, 1 cM is roughly equivalent to 1 megabase (Mb) of DNA in humans, although this can vary widely due to hot and cold spots of recombination.) The cM distances are based on genetic markers mapped by Génethon which provide boundaries for radiation hybrid markers whose sequences were included in each of the clusters. Diseases associated with the public and Incyte sequences located within the indicated intervals are also reported in the Invention section where applicable. Human genome maps and other resources available to the public, such as the NCBI "GeneMap'99" World Wide Web site (~~<http://www.ncbi.nlm.nih.gov/genemap/>~~) ([ncbi.nlm.nih.gov/genemap/](http://www.ncbi.nlm.nih.gov/genemap/)), can be employed to determine if previously identified disease genes map within or in proximity to the intervals indicated above.